

jc858 U.S. PTO  
10/007267  
12/03/01

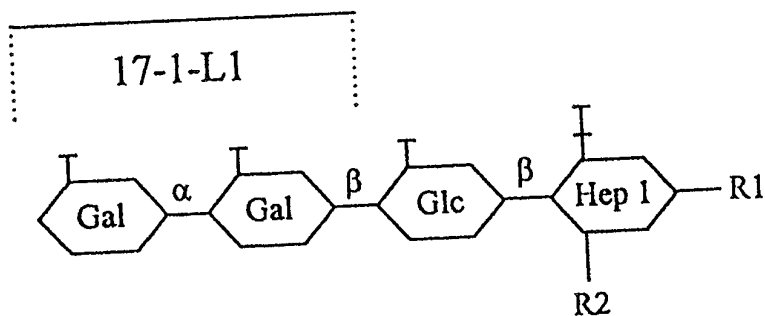
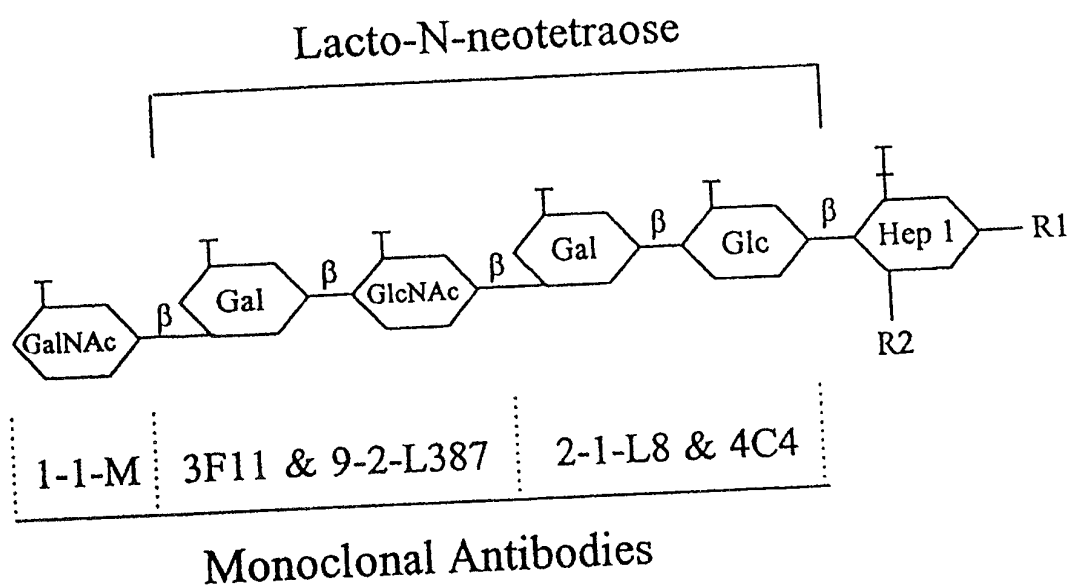


FIG. 1

## LOS Locus

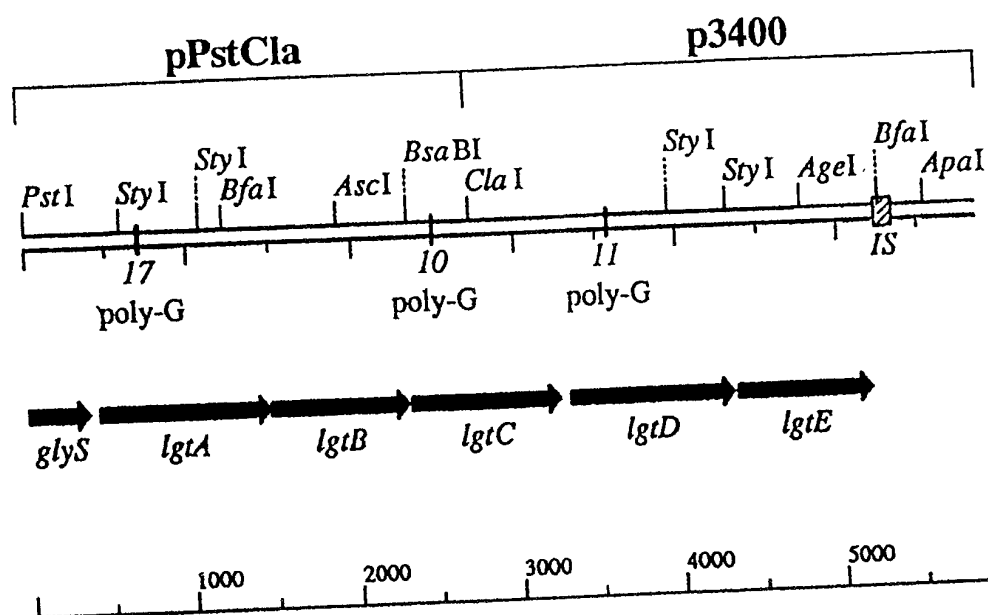


FIG.2A

## FIG. 2B-1

SOURCE Neisseria gonorrhoeae.  
 ORGANISM Neisseria gonorrhoeae  
 source 1..5859

CDS  
 <1..381  
 /gene="glyS"  
 /codon\_start=1  
 /transl\_table=11  
 /product="glycyl tRNA synthetase beta chain"

/translation="LQAVAVFKQLPEAAALAAANKRVQNLLKKADAALGEVNESLLQQ  
 DEEKALYAAAQGLQPKIAAAVAEGNFRTALSELASVKPQVDAFFDGMVMAEDAAVKQ  
 NRLNLLNRLAEQMNAVADIALLGE"

CDS  
 445..1491  
 /gene="lgtA"  
 /codon\_start=1  
 /function="adds GlcNAc to lacto-N-neotetraose chain of  
 gonococcal LOS"  
 /evidence=experimental  
 /transl\_except=(pos:445..447,aa:Met)  
 /transl\_table=11  
 /product="glycosyl transferase"

/translation="MQPLVSVLICAYNVEKYFAQSLAAVVNQTWRLDILIVDDGSTD  
 GTLAIKDFQKRDSRIKILAQANSGLIPSNLIGLDELA KSGGGEYIARTDADDIA  
 SPGWIEKIVGEMEKDRSIIAMGAWLEVLSEKDGNRRLARHHKHKIWKKPTRHEDIAA  
 FFPFGNPIHNNTMIMRRSVIDGGLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKY  
 RLHANQVSSKHSVRQHEIAQGIQKTARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEK  
 DLPEEDFERARRFLYQCFKRTDTPPSGAWLDFEAADGRMRRLFTLRQYFGILYRLIKNR  
 RQARSDSAGKEQEI"

## FIG.2B-2

CDS

1491..2330  
 /gene="lgtB"  
 /codon\_start=1  
 /function="adds second galactose to the lacto-N-tetraose  
 chain in LOS"  
 /evidence=experimental  
 /product="glycosyl transferase"

/translation="MQNHVISLASAAERRAHIAATFGSRGIPFQFFDALMPSERLERA  
 MAELVPGLSAHPYLSGVEKACFMASHAVLWEQALDEGVPIAVFEDDVLGEGAEQFLA  
 EDTWLQERFDPDSAFVVRLETMTFMHVLTPSGVADYGGRAFPILLESEHCCTAGYIISR  
 KAMRFFLDRAVLPPERLHPVDLMMFGNPDDREGMPVCQLNPALCAQELHYAKFHDQN  
 SALGSLIEHRRRLNRKQQWRDSPANTFKHRLIRALTIGREREKRRQRREQLIGKIIIV  
 PFQ"

CDS

2342..3262  
 /gene="lgtC"  
 /codon\_start=1  
 /function="adds galactose alpha(1-4) to Gal-Glc in  
 gonococcal LOS"  
 /evidence=experimental  
 /transl\_table=11  
 /product="glycosyl transferase"

/translation="MDIVFAADDNYAAVLCVAAKSVEAAHPDTEIRFHVLDAGISEEN  
 RAAVAANLRGGNIRFIDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCDKVLVLD  
 TDVLVRDGLKPLWDTDLGGNWVGACIDLFEVERQEGYKQKIGMADGEYFYNAGVLLINL  
 KKWRRHDI FKMSCEWVEQYKDVMMQYQDDIILNGLFKGGVCYANSRNFNPTNYAFMAN  
 GFASRHTDPLYLDRNTAMPVAVSHYCGSAKFPWHRDCTVWGAERFTELAGSLTTVPPEE  
 WRGKLAVPPTKCMQLQRWRKKLSARFLRKIY"

## FIG.2B-3

```

CDS
3322..4335
/gene="lgtD"
/codon_start=1
/function="adds terminal GalNAc to lacto-N-neotetraose
chain of LOS"
/evidence=experimental
/transl_except=(pos:3322..3324,aa:Met)
/transl_table=11
/product="glycosyl transferase"

/translation="MQPLVSVLICAYNAEKYFAQSLAAVVGQWTRNLDILIVDDGSTD
GTPAIARHFQEQDGRIRIISNPNLGFIAISNLIGLDELAKSGGGEYIARTDADDIASP
GWIEKIVGEMEKDRSIIAMGAWLEVLSENNKSVLAAIARNGAIWDKPTRHEDIVAVF
PFGNPIHNNMTIMRRSVIDGGLRFPDPAITHAEDYKFWYEAGKLGRLAYYPEALVKYRF
HQDQTSKYNLQQRRTAWKIKEEIRAGYWKAAAGIAGADCLNYGLLKSTAYALYEKAL
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RSY"
CDS
4354..5196
/gene="lgtE"
/codon_start=1
/function="adds first galactose to lacto-N-neotetraose
chain of LOS"
/evidence=experimental
/transl_table=11
/product="glycosyl transferase"

/translation="MQNHVISLASAERRAHIADTFGSRGIPFQFFDALMPSEERLEQA
MAELVPGLSAHPYLSGVEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLGEGAEQFLA
EDTWLEERFDKDSAFIVRLETMTFAKVIVRPDKVLNYENRSFPLLESEHCGTAGYIISR
EAMRFFLDRAFVLPPERIKAVDLMFTYFFDKEGMPVYQVSPALCTQELHYAKFLSQN
SMLGSDLEKDREQRRHRRSLKVMFDLKRALGKFGREKKRMRERQRAELEKVIYGRRV
ILFK"

```

## FIG.2B-4

BASE COUNT		1412 a	1462 c	1661 g	1324 t
ORIGIN					
1	ctgcaggccg	tcgccgtatt	caaacaactg	ccgaagccg	ccgcgctcgc
61	aaacgcgtgc	aaaacctgct	gaaaaaagcc	gatgcgcgt	tgggcgaagt
121	ctgctgcaac	aggacgaaga	aaaagccctg	tacgctgccg	cgcaagggtt
181	attgcccgcg	ccgtcgccga	aggcaatttc	cgaaccgcct	tgccggaact
241	aagccgcagg	ttgatgcctt	cttcgacggc	gtgatggtga	tgggcgaaga
301	aaacaaaacc	gcctgaacct	gctgaaccgc	ttggcagagc	agatgaacgc
361	atcgcgcttt	tgggcgagta	accgttgtac	agtcctgaag	ccgtctgaag
421	gcatcaaat	atcgggagag	taaatggcag	cctttagtca	gcgtattgat
481	aacgtagaaa	aatattttgc	ccaatcatta	gccgcgcgtc	tgaatcagac
541	ttggatat	tgattgtcga	tgacggctcg	acagacggca	cacttgccat
601	tttcaaaagc	gggacagccg	tatcaaaatc	cttgacacaag	ctcaaaatc
661	ccctctttaa	acatcgggct	ggacgaattg	gcaaagtcgg	gggggggggg
721	attgcgcgca	ccgatgccga	cgatatggcc	tccccgggct	ggattgagaa
781	gagatggaaa	aagaccgcag	catcattgcg	atgggcgcgt	ggctggaaagt
841	gaaaaggacg	gcaaccggct	ggcgcggcac	cacaaacacg	gcaaaatttg
901	accgggcacg	aagacatcgc	cgcctttttc	cctttcggca	acccatata
961	atgattatgc	ggcgcagcgt	cattgacggc	ggtttgcgtt	acgacaccca
1021	gcggaagatt	accaattttg	gtacgatgtc	agcaaatggg	gcaggctggc
1081	gaagccttgg	tcaaataccg	ccttcacgcc	aatcagggtt	catccaaaca
1141	caacacgaaa	tcgcgcaagg	catccaaaaa	accgcccaga	acgatttttt
1201	ggttttaaaa	cccgggttcga	cagcctagaa	taccgcccga	caaaagcagc
1261	ctgcccggaga	aggattttgc	ggaagaagat	tttgaacgcg	ccgcgcgggt
1321	tgcttcaaac	ggacggacac	gccgccctcc	ggcgcgtggc	tggaattcgc
1381	aggatgaggg	ggctgtttac	cttgaggcaa	tacttcggca	ttttgtaccg
1441	aaccgcccgc	aggcgcggtc	ggattcggca	gggaaagaac	aggagattta
1501	acgttatcag	cttggcttcc	gccgcagaa	gcaggggcgca	cattgcgcga
1561	gtcgcggcat	cccgttccag	tttttcgacg	cactgatggc	gtctgaaagg

FIG.2B-5

1621	caatggcgga	actcgtcccc	ggcttgctcg	cgaccccta	tttgagcgga	gtggaaaaag
1681	cctgctttat	gagccacgcc	gtattgtggg	aacaggcatt	ggacgaaggc	gtaccgtata
1741	tcgcccgtatt	tgaagatgat	gtcttactcg	gcgaaggcgc	ggacagtttc	cttgccgaag
1801	atacttggct	gcaagaacgc	tttgaccccc	attccgcctt	tgtcgtccgc	ttggaacga
1861	tgtttatgca	ctcctgacc	tcgcccctcg	gcgtggcgga	ctacggcggg	cgcgcccttc
1921	cgctttttgga	aagcgaacac	tcggggacgg	cggtctatat	tatttccga	aaggcgatgc
1981	gtttttttctt	ggacaggttt	gccgttttgc	cgcccgaacg	cctgcacct	gtcgatttga
2041	tgatgttcgg	caaccctgac	gacagggaag	gaatgccggt	ttgccagctc	aatcccgcct
2101	tgtgcgcca	agagctgcat	tatgccaaagt	ttcacgacca	aaacagcgca	ttgggagagcc
2161	tgatcgaaca	tgaccgcgcg	ctgaaccgca	aacagcaatg	gcgcatctcc	cccgcacaac
2221	cattcaaac	ccgcctgac	cgcgcccttga	ccaaaatcgg	cagggaagg	gaaaaacgcc
2281	ggcaaaaggcg	cgaacagtta	atcggcaaga	ttattgtgcc	tttccaataa	aaggagaaaa
2341	gatggacatc	gtatttgcgg	cagacgacaa	ctatgccgcg	tacctttgcg	ttgcggcaaa
2401	aagcgtggaa	gcggcccatc	ccgatacgg	aatcaggttc	cacgtccctcg	atgccggcat
2461	cagtaggaa	aaccgggcgg	cggttgccgc	caatttgcgg	ggggggggta	atatccgctt
2521	tatagacgta	aaccgcgaag	atttcgcccg	ctccccctta	aacatcaggc	acatttccat
2581	tacgacttat	gcccgcctga	aattgggcga	atacatggcc	gattgcgaca	aagtccctga
2641	tctggatacg	gacgtattgg	tcagggacgg	cctgaagccc	ttatgggata	ccgatttggg
2701	cggtaaactgg	gtcggcgcg	gcatcgattt	gtttgtcgaa	aggcagggaag	gatacaaca
2761	aaaaatcgg	atggcgagcg	gagaatat	tttcaatgcc	ggcgtattgc	tgatcaacct
2821	gaaaaagtgg	cggcggcacg	atattttcaa	aatgtccctgc	gaatgggtgg	acaatacaaa
2881	ggacgtgatg	caatatcagg	atcaggacat	tttgaacggg	ctgttttaag	gcggggtgtg
2941	ttatgcgaac	agccgtttca	actttatgcc	gaccaattat	gccttttatgg	cgaaacgggtt
3001	tcgctccccg	cataccgacc	cgctttacct	cgaccgtacc	aatacggcga	tgcccgtcgc
3061	cgtcagccat	tattgcggct	cggaacagcc	gtggcacagg	gactgcaccg	tttgggggtgc
3121	ggaacgtttc	acagagttag	ccggcagcct	gacgaccgtt	ccgaaagaat	ggcgcggaac
3181	acttgcgctc	ccgccgacaa	agtgtatgct	tcaagatgg	cgcaaaaagc	tgctcgccag
3241	attcttacgc	aagatttatt	gacggggcag	gccgtctgaa	gccttcagac	ggcatcggac
3301	gtatcggaac	ggagaaacgg	attgcagcct	ttagtcagcg	tattgatttg	cgctacaac
3361	gcagaaaaat	attttgcccc	atcattggcc	gccgtagtgg	ggcagacttg	gcgcaacttg

FIG.2B-6

3421 gataatttga ttgtcgatga cggctcgacg gacggcacgc cggccattgc cggcatttc  
3481 caagaacagg acggcaggat caggataatt tccaatcccc gcaatttggg ctttatcgcc  
3541 tctttaaaca tcgggctgga cgaattggca aagtcggggg ggggggaata tattgcgcgc  
3601 accgatgccg acgatatatgc acgatatatgc ctcccccggc tggattgaga aaatcgtggg cgagatggaa  
3661 aaagaccgca gcatcatgac gcatcatgac gatggcgcg tggttggaa tttgtcggg agaaaaaat  
3721 aaaagcgtgc ttgcccgcac ttgcccgcac ggcgcaattt gggacaacac gaccggcat  
3781 gaagacattg tcgcccgttt tcgcccgttt ggcgcaattt ggcgcaacac gatgattatg  
3841 aggcgcagcg tcattgacgg tcattgacgg cggtttgcgg ttcgatccag cctatatcca gccgaagac  
3901 tataagtatt ggtacgaagc ggtacgaagc cggcaaaactg ggcaggctgg cttattatcc cgaagccttg  
3961 gtcaaatacc gcttccatca agaccagact tcttccaaat acaacctgca acagcgagg  
4021 acggcgtgga aaatcaaga agaaatcagg gcgggggtatt ggaaggcgcc aggcatagcc  
4081 gtggggcgcg actgcctgaa ttacgggctt ttgaaatcaa ttgaaatcaa cggcataatgc gttgtacgaa  
4141 aaagccttgt ccggacagga tatcggatgc ctccgcctgt tcctgtacga atatttcttg  
4201 tcgttggaaa agtatcttt ccgcaccgca atataggaaa atcctgaaaa cagcgttat  
4261 aagctgtttg ccgcaccgca aacaggataa acatgcaaa atcctgtaac gacttggct  
4321 taccgcagct attgaaaccg gcacattgcc gataccttcg gacgtcgcgg catccgttc  
4381 tccgcgcagc acgcactgat gcgctctgaa aggcgggaa aggcgatggc ggaactcgtc  
4441 cagtttttcg ccgcgcaccg ctatttgagc ggtctgccc ttccttggaa atagagccac  
4501 ccggccttgt gggaaacagg gttggatgaa ggtctgccc ttccttggaa atagagccac  
4561 gccgtattgt tcggcgaaag cgttgatgaa ggtctgccc ttccttggaa atagagccac  
4621 gacgttttac aggatccgc ataatatgaa aacctgcat ttccttggaa atagagccac  
4681 cgttttgaca aggatccgc ataatatgaa aacctgcat ttccttggaa atagagccac  
4741 gtcagaccgg ataatatgaa aacctgcat ttccttggaa atagagccac  
4801 cattgtggga cggctggcta taccatttcg cgtgagcga tgcggtttt cttggacagg  
4861 ttgcccgttt tgccgccaga ggggatgcc tgtttatcag gttagtcagg ccttatgtac ccaagaattg  
4921 ttgataagg aggggatgcc tcaaaacagt atgttgggta ggcatttggg cgaacttgg  
4981 cattatgcca agtttctcag ccgttcgttg aagtgatgt ttgacttggg aaagatagg  
5041 gaacaaggaa gaagacaccg ccgttcgttg aagtgatgt ttgacttggg aaagatagg  
5101 ggtaaattcg gtagggaaaa atggagcgtc aaagcaggc ggagccttg  
5161 aaagtattcg gcagcggggt catattgttc aaatagtttg tgtaaaatat aggggattaa



## FIG.2B-7

5221 aatcagaaat ggacacactg tcattcccgc gcaggcggga atctagggtct ttaaacttcg  
5281 gttttttccg ataaattctt gccgcattaa aattccagat tcccgccttc gcggggatga  
5341 cggcggggg atgttgctt ttccggataa aatcccgtgt tttttcatct gctaggtaaa  
5401 atcgcccaa agcgtctgca tcgcggcgat gccggcttca aatgacctgtt gtctctcctg  
5461 aatccgtttt ccgagtgtaa ccgcctgaaa gcccaccat aaagacgatt gcgccggacg ggtggcggat  
5521 ttctgtccag ccgccttcgg ggttgatgct cataatcagc ttggtgtttt cagacggcat  
5581 gtccgcgagt ttgcaggcgc agccgatgat gggcagtacg gggggaaacgg tgttcctgcc  
5641 ttgttcgagt gcttcacggt cagcggaga tgacgatttc ctgccagcgt gcgaggcgtt tggcggcgcg  
5701 gctttgttcg cacttcgagt aggcggacga tgcagcgttc gctgatgacg ggctgtatgg cggttacgcc  
5761 ttctccgtcg aggcggacga tgcagcgttc gctgatgacg ggctgtatgg cggttacgcc  
5821 ggttcgacg cttttttgca ggtgaaatc catgcgac



FIG. 3B

1gtB 1 MQNHV ISLASAAERRAHIA DTFGSRGIPFQFFDALMPSERLEQAMAE LVP 50  
|||||  
1gtE 1 MQNHV ISLASAAERRAHIA DTFGSRGIPFQFFDALMPSERLEQAMAE LVP 50  
|||||  
1gtB 51 GLSAHLYLSGVEKACFMSH AVLWEQALDEGLPYIAVFEDD VLLGEGAEQF 100  
|||||  
1gtE 51 GLSAHPYLSGVEKACFMSH AVLWEQALDEGLPYIAVFEDD VLLGEGAEQF 100  
|||||  
1gtB 101 LAEDTWLQERFDPDSAFVVRLETMFMHVL TSPSGVADYGGRAFPLLESEH 150  
|||||  
1gtE 101 LAEDTWLEERFDKDSAFIVRLETMFAKVI VRPDKVLNYENRSFPLLESEH 150  
|||||  
1gtB 151 CGTAGYIISRKAMRFFLD RFAVLPPERLHPVDLMMFGNPDDREGMPVCQL 200  
|||||  
1gtE 151 CGTAGYIISREAMRFFLD RFAVLPPERIKAVDLM MFTYFFDKEGMPVYQV 200  
|||||

FIG.4A

1gtB 201 NPALCAQELHYAKFHDQNSALGSLIEHRRRLNRKQQRDSPANTFKHRLI 250  
          . . . . .  
1gtE 201 SPALCTQELHYAKFLSQNSMLGSDLEKD . . . . . REQGRRHRRSLKVMFDLK 246  
          . . . . .  
1gtB 251 RALTKIGREREKRRKRR . . . . . EQTIGKIIVPFQ 279  
          . . . . .  
1gtE 247 RALGKFGREKKRMERQORQAELEKVYGRRVILFK 280  
          . . . . .

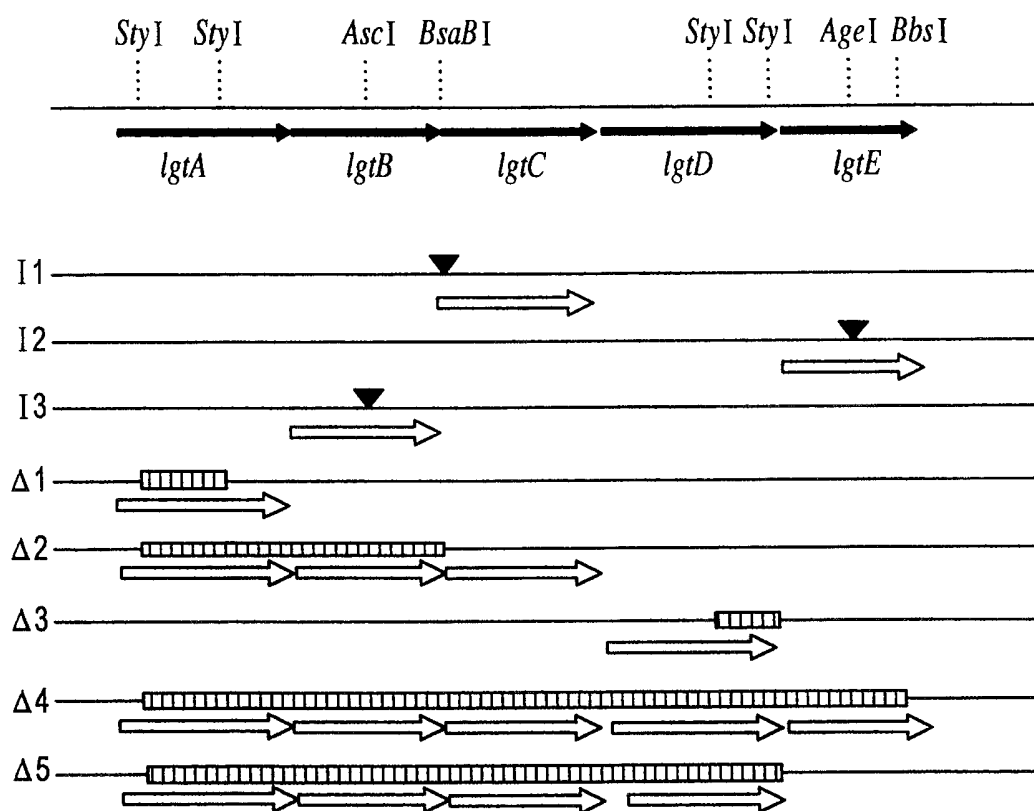
FIG.4B

rfaI 29 LDIAYGTDKNFLFGCGISIASILKYNEGSRLCFHIFTDYFGDDDRKYFDA 78  
1 MDIVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEENRAAVAA 50  
79 LALQYKTRIKIYLINGDRLRSLP.STKNWTHAIYFRFVIADYFINKAPKV 127  
51 .NLRGGNIRFIDVNPEDFAGFPLNIRHISITTYARLKLGEY.IADCCKV 98  
128 LYLDADIICQGTIEPLINFSPDDKVAMVV...TEGQADWWEKRAHSLGV 174  
99 LYLDTDVLVRDGLKPLWDTDLGGNWWGACIDL FVERQEGYKQK....IGM 144  
175 AGIAKGYFNSGFLINTAQWAAQQVSARAIAMLNEPEIIKKITHPDQDVL 224  
145 AD.GEYFYNAGVLLINLKKWRRHDIFKMSCEWVEQYKDV MQ..YQDQDIL 191

FIG.5A



FIG.6





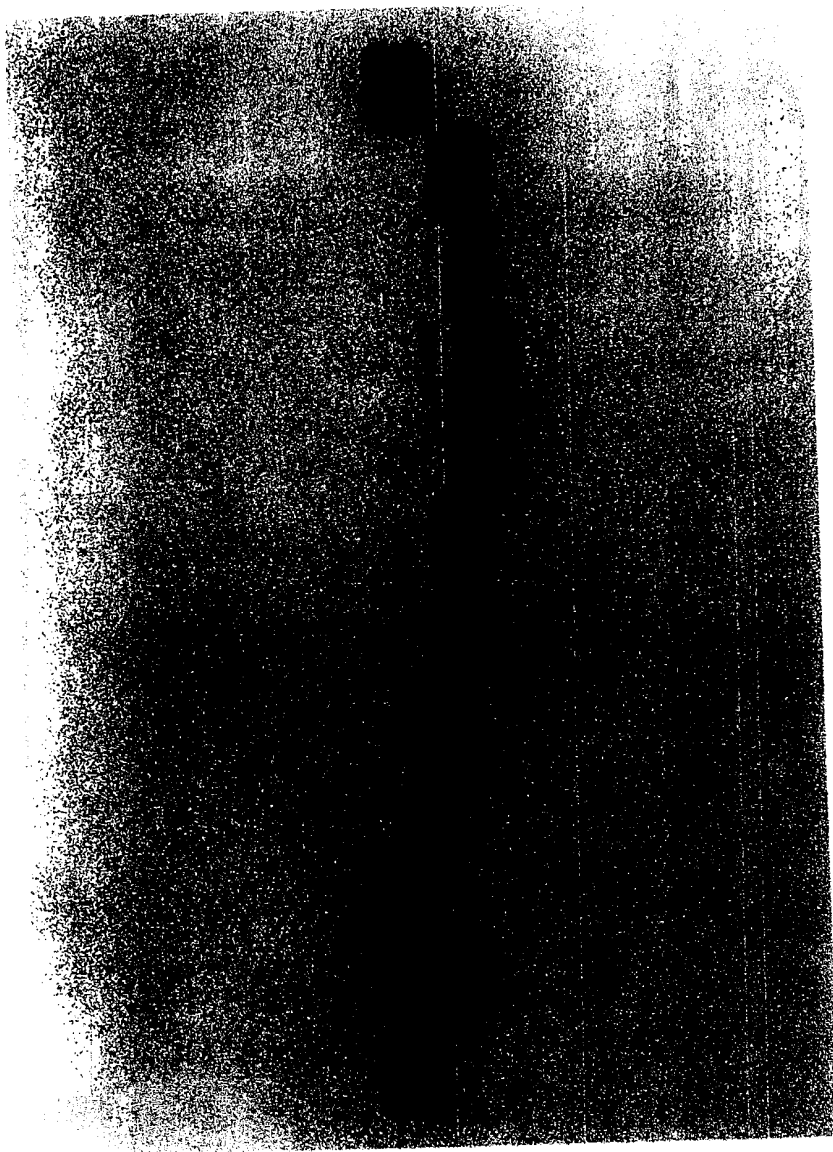


FIG. 7

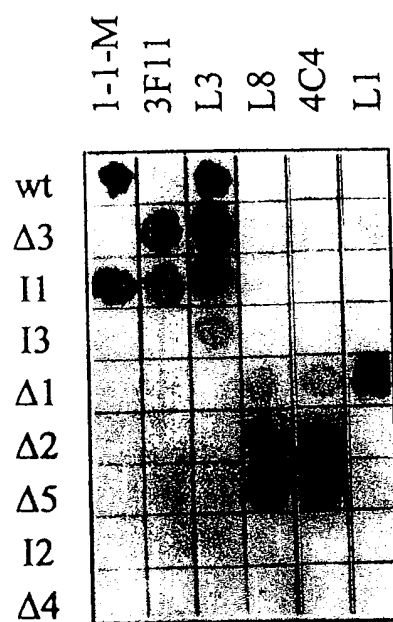


FIG.8